

WEST Search History

9/9/03
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DATE: Tuesday, September 09, 2003

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DB=USPT; PLUR=YES; OP=AND

L1	6551795.pn.	1	L1
L2	mur or murd or mur-d	310	L2
L3	L2 and pseudomon\$	63	L3
L4	L2 same pseudomon\$	8	L4
L5	UDP-N-acetylmuramoylalanine-D-glutamate near3 ligase	4	L5
L6	('6593114' '6211161' '6528289' '6506581')[PN]	4	L6
L7	UDP-MurNAc-L-Ala	13	L7

END OF SEARCH HISTORY

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☐ 1. 6593114. 20 Oct 97; 15 Jul 03. Staphylococcus aureus polynucleotides and sequences. Kunsch; Charles A., et al. 435/91.41; 435/252.3 435/254.11 435/257.2 435/320.1 435/325 435/91.4 536/23.7. C12N015/64 C07H021/04.

☐ 2. 6528289. 23 Aug 00; 04 Mar 03. Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof. Fleischmann; Robert D., et al. 435/91.41; 435/252.3 435/320.1 435/6 536/23.1 536/23.7. C12N015/64.

☐ 3. 6506581. 25 Apr 00; 14 Jan 03. Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof. Fleischmann; Robert D., et al. 435/69.1; 435/252.3 435/320.1 435/69.3 435/91.41 536/23.7. C12N001/21 C12N015/31 C12N015/63.

☐ 4. 6211161. 19 Mar 99; 03 Apr 01. UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase (MURD) of staphylococcus aureus. Beattie; David T, et al. 514/44; 435/252.3 435/254.11 435/320.1 435/325 435/455 435/471 435/69.1 536/23.1 536/23.2 536/23.4 536/23.7. A61K048/00 C07H021/00 C12N015/31 C12N015/52 C12N015/63.

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Terms	Documents
UDP-N-acetylmuramoylalanine-D-glutamate near3 ligase	4

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WEST**Search Results - Record(s) 1 through 4 of 4 returned.**

L6: Entry 1 of 4

File: USPT

Jul 15, 2003

US-PAT-NO: 6593114

DOCUMENT-IDENTIFIER: US 6593114 B1

TITLE: Staphylococcus aureus polynucleotides and sequences

DATE-ISSUED: July 15, 2003

US-CL-CURRENT: 435/91.41, 435/252.3, 435/254.11, 435/257.2, 435/320.1, 435/325, 435/91.4, 536/23.7INT-CL: [07] C12 N 15/64, C07 H 21/04

L6: Entry 2 of 4

File: USPT

Mar 4, 2003

US-PAT-NO: 6528289

DOCUMENT-IDENTIFIER: US 6528289 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

DATE-ISSUED: March 4, 2003

US-CL-CURRENT: 435/91.41, 435/252.3, 435/320.1, 435/6, 536/23.1, 536/23.7INT-CL: [07] C12 N 15/64

L6: Entry 3 of 4

File: USPT

Jan 14, 2003

US-PAT-NO: 6506581

DOCUMENT-IDENTIFIER: US 6506581 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

DATE-ISSUED: January 14, 2003

US-CL-CURRENT: 435/69.1, 435/252.3, 435/320.1, 435/69.3, 435/91.41, 536/23.7

INT-CL: [07] C12 N 1/21, C12 N 15/31, C12 N 15/63

L6: Entry 4 of 4

File: USPT

Apr 3, 2001

US-PAT-NO: 6211161

DOCUMENT-IDENTIFIER: US 6211161 B1

TITLE: UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase (MURD) of staphylococcus aureus

DATE-ISSUED: April 3, 2001

US-CL-CURRENT: 514/44, 435/252.3, 435/254.11, 435/320.1, 435/325, 435/455, 435/471, 435/69.1,
536/23.1, 536/23.2, 536/23.4, 536/23.7

INT-CL: [07] A61 K 48/00, C07 H 21/00, C12 N 15/31, C12 N 15/52, C12 N 15/63

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L4: Entry 7 of 8

File: USPT

Nov 10, 1998

DOCUMENT-IDENTIFIER: US 5834270 A

TITLE: Biosynthetic gene murD from streptococcus pneumoniae

Detailed Description Text (35):

In general, prokaryotes are used for cloning DNA sequences and for constructing the vectors of the present invention. Prokaryotes are also employed in the production of the MurD protein. For example, the Escherichia coli K12 strain 294 (ATCC No. 31446) is particularly useful for the prokaryotic expression of foreign proteins. Other strains of E. coli, bacilli such as Bacillus subtilis, enterobacteriaceae such as Salmonella typhimurium or Serratia marcescans, various Pseudomonas species and other bacteria, such as Streptomyces, may also be employed as host cells in the cloning and expression of the recombinant proteins of this invention.

WEST**End of Result Set**

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L4: Entry 8 of 8

File: USPT

Oct 28, 1997

US-PAT-NO: 5681694

DOCUMENT-IDENTIFIER: US 5681694 A

TITLE: MurD protein method and kit for identification of inhibitors

DATE-ISSUED: October 28, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Hoskins; Jo Ann	Indianapolis	IN		
Peery; Robert Brown	Brownsburg	IN		
Skatrud; Paul Luther	Indianapolis	IN		
Wu; Chyun-Yeh Earnest	Indianapolis	IN		

US-CL-CURRENT: 435/4; 435/183, 435/184**CLAIMS:**

We claim:

1. A substantially pure MurD protein from *Streptococcus pneumoniae* having the amino acid sequence: ##STR2## which is SEQ ID NO 2.
2. A method for identifying inhibitory compounds of *Streptococcus pneumoniae* MurD protein activity, comprising the steps of:
 - a) admixing in a suitable reaction buffer
 - i) a substantially pure MurD protein as claimed in claim 1;
 - ii) a suitable substrate;
 - iii) a test inhibitory compound;
 - b) measuring by any suitable means the amount of product formed; and
 - c) comparing the amount of product formed with a control in which no test inhibitory compound is present.
3. A method, as in claim 2 wherein the substrate of step (a) (ii) comprises UDP-MurNAc-L-Ala.

4. A method, as in claim 2 wherein the amount of product formed at step (b) is determined by HPLC.

5. A kit useful for identifying inhibitors of stem peptide biosynthesis said kit comprising in separate containers:

- a) a substantially pure MurD protein, as claimed in claim 1; and
- b) a suitable substrate for said protein.

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Search Results - Record(s) 1 through 4 of 4 returned.

☐ 1. Document ID: US 6593114 B1

L5: Entry 1 of 4

File: USPT

Jul 15, 2003

DOCUMENT-IDENTIFIER: US 6593114 B1

TITLE: Staphylococcus aureus polynucleotides and sequences

Detailed Description Paragraph Table (27):

2406 1 227 3 gi.vertline.1041785 rhoptry protein [Plasmodium yoelii] 63 33 225 2961 2 136 360
 gi.vertline.312443 carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus 63 52 225 aldolyticus]
 2965 1 1 402 gi.vertline.1407784 orf-1; novel antigen [Staphylococcus aureus] 63 50 402 2987 1 293 3
 gi.vertline.1224069 amidase [Moraxella catarrhalis] 63 35 291 2994 1 135 4 gi.vertline.836646
 phosphoribosylformimino-praia ketoisomerase [Rhodobacter 63 51 132 phaeroides] 3043 1 252 64
 gi.vertline.1480237 phenylacetaldehyde dehydrogenase [Escherichia coli] 63 40 189 3078 1 400 191
 gi.vertline.1487982 intrinsic membrane protein [Mycoplasma hominis] 63 36 210 3139 1 2 217
 gi.vertline.439126 glutamate synthase (NADPH) [Azospirillum brasilense] 63 47 216
 pir.vertline.A49916.vertline.A49916 glutamate synthase (NADPH) (EC 1.4.1.13) - zospirillum brasilense 3625 1
 398 3 gi.vertline.623073 ORF360; putative [Bacteriophage LL-H] 63 48 396 3658 1 1 399 gi.vertline.1303697
 Yrka [Bacillus subtilis] 63 37 399 3659 1 3 395 gi.vertline.1256135 YbbF [Bacillus subtilis] 63 48 393 3783 1
 361 2 gi.vertline.1256902 Pyruvate decarboxylase isozyme 2 (Swiss Prot. accession number 63 34 360 P16467)
 [Saccharomyces cerevisiae] 3900 1 171 4 sp.vertline.P10537.vertline.AMYB.sub.-- BETA-AMYLASE (EC 3.2.1.2)
 (1,4-ALPHA-D-GLUCAN 63 54 168 MALTOHYDROLASE). 4309 1 3 176 pir.vertline.A37967.vertline.A379
 neural cell adhesion molecule Ng-CAM precursor - chicken 63 57 174 4367 1 1 195 gi.vertline.1321932 Per6p
 gene product [Pichia pastoris] 63 30 195 4432 1 1 312 gi.vertline.151259 HMG-CoA reductase (EC 1.1.1.88)
 [Pseudomonas mevalonii] 63 51 312 pir.vertline.A44756.vertline.A44756 hydroxymethylglutaryl-CoA reductase
 (EC 1.1.1.88) Pseudomonas sp. 4468 1 6 308 gi.vertline.296464 ATPase [Lactococcus lactis] 63 36 303 33 3
 1411 2400 gi.vertline.153675 tagatose 6-P kinase [Streptococcus mutans] 62 44 990 36 9 5985 6218
 gi.vertline.1490521 hMSH3 [Homo sapiens] 62 51 234 37 1 2 721 gi.vertline.1107531 ceuE gene product
 [Campylobacter coli] 62 33 720 38 15 10912 11589 gi.vertline.1222058 H. influenzae predicted coding region
 HIN1279 [Haemophilus 62 38 678 influenzae] 38 25 19526 20329 gi.vertline.695280 ORF2 [Alcaligenes
 eutrophus] 62 41 804 57 2 1780 1037 gi.vertline.471234 orf1 [Haemophilus influenzae] 62 55 744 57 9 6350
 6054 gi.vertline.508174 EIIB domain of PTS-dependent Gat transport and phosphorylation 62 35 297
 [Escherichia coli] 58 1 2 559 gi.vertline.755152 highly hydrophobic integral membrane protein [Bacillus
 subtilis] 62 34 558 sp.vertline.P42953.vertline.TAGG_BACSU TEICHOIC ACID TRANSLOCATION
 PERMEASE PROTEIN AGG. 67 10 8250 9014 gi.vertline.470683 Shows similarity with ATP-binding proteins
 from other ABC- 62 34 765 transport perons, Swiss Prot Accession Numbers P24137, P08007, P04285,
 P24136 [Escherichia coli] 69 8 7494 6673 gi.vertline.46816 actVA 4 gene product [Streptomyces coelicolor]

62 44 822 80 3 1320 847 gi.vertline.39993 UDP-N-acetylmuramoylalanine--D-glutamate ligase [Bacillus 62 43
 474 subtilis] 87 7 7034 9205 gi.vertline.217191 5'-nucleotidase precursor [Vibrio parahaemolyticus] 62 48
 2172 100 3 3089 2127 gi.vertline.1511047 phosphoglycerate dehydrogenase [Methanococcus jannaschii] 62 42
 963 102 1 2 520 gi.vertline.153655 mismatch repair protein [Streptococcus pneumoniae] 62 34 519
 pir.vertline.C28667.vertline.C28667 DNA mismatch repair protein hexA - Streptococcus pneumoniae 112 2 466
 1068 gi.vertline.153741 ATP-binding protein [Streptococcus mutans] 62 37 603 114 7 6855 7562
 gi.vertline.1204866 L-fucose operon activator [Haemophilus influenzae] 62 38 708 116 4 5633 4443
 gi.vertline.677947 AppC [Bacillus subtilis] 62 37 1191 124 8 6004 5153 gi.vertline.853777 product similar to E.
 coli PRFA2 protein [Bacillus subtilis] 62 44 852 pir.vertline.S55438.vertline.S55438 ywK protein - Bacillus
 subtilis sp.vertline.P45873.vertline.HEMK_BACSU POSSIBLE PROTOPORPHYRINOGEN OXIDASE (EC
 .3.3.--). 148 1 24 554 gi.vertline.467456 unknown [Bacillus subtilis] 62 50 531 149 20 6725 5859
 gi.vertline.1205807 replicative DNA helicase [Haemophilus influenzae] 62 41 867 163 3 1153 803
 gi.vertline.40067 X gene product [Bacillus sphaericus] 62 42 351 164 15 14673 15632 gi.vertline.42219 P35
 gene product (AA 1-314) [Escherichia coli] 62 38 960 165 2 1166 1447 gi.vertline.403936 phenylalanyl-tRNA
 synthetase alpha subunit (Gly294 variant) 62 38 282 [unidentified cloning vector] 166 2 2084 5089
 gi.vertline.308861 GTG start codon [Lactococcus lactis] 62 44 3006 171 1 614 3 gi.vertline.1046053
 hypothetical protein (SP:P32049) [Mycoplasma genitalium] 62 41 612 183 1 1310 99 gi.vertline.143045 hemY
 [Bacillus subtilis] 62 45 1212 200 1 3 956 gi.vertline.142439 ATP-dependent nuclease [Bacillus subtilis] 62 32
 954 237 2 935 1966 gi.vertline.41695 hisC protein [Escherichia coli] 62 44 1032 261 3 2605 1202
 gi.vertline.143121 ORF A; putative [Bacillus firmus] 62 42 1404 299 8 4477 4719 gi.vertline.467441 expressed
 at the end of exponential growth under conditions in which 62 47 243 the enzymes of the TCA cycle are
 repressed [Bacillus subtilis] gi.vertline.467441 expressed at the end of exponential growth under conditions in
 which the enzymes of the TCA cycle are repressed Bacil 304 6 3819 2620 gi.vertline.153015 FemA protein
 [Staphylococcus aureus] 62 43 1200 324 1 2 262 gi.vertline.142717 cytochrome aa3 controlling protein
 [Bacillus subtilis] 62 30 261 pir.vertline.A33960.vertline.A33960 cta protein - Bacillus subtilis
 sp.vertline.P12946.vertline.CTAA_BACSU CYTOCHROME AA3 CONTROLLING PROTEIN. 325 2 269 1207
 gi.vertline.581088 methionyl-tRNA formyltransferase [Escherichia coli] 62 39 939 332 6 4631 4368
 gi.vertline.1499960 uridine 5'-monophosphate synthase [Methanococcus jannaschii] 62 36 264 355 1 2 370
 gi.vertline.145925 fecB [Escherichia coli] 62 32 369 365 8 6628 6804 gi.vertline.413943 ipa-19d gene
 product [Bacillus subtilis] 62 54 177 369 2 1626 508 pir.vertline.A43577.vertline.A435 regulatory protein
 pfoR - Clostridium perfringens 62 42 1119 370 1 34 264 gi.vertline.40665 beta-glucosidase [Clostridium
 thermocellum] 62 37 231 415 3 2709 3176 gi.vertline.1205401 transport ATP-binding protein [Haemophilus
 influenzae] 62 35 468 429 1 790 2 gi.vertline.1046024 Na⁺ ATPase subunit J [Mycoplasma genitalium] 62 40
 789 444 2 704 1369 gi.vertline.581510 nodulation gene; integral membrane protein; homology to Rhizobium 62
 37 666 eguminosarum nodI [Rhizobium loti] 477 2 751 1869 pir.vertline.A48440.vertline.A484 ring-infected
 erythrocyte surface antigen 2, RESA-2 - 62 44 1119 Plasmodium falciparum 485 1 241 1707 gi.vertline.17934
 betaine aldehyde dehydrogenase [Beta vulgaris] 62 43 1467 487 3 1141 1311 gi.vertline.149445 ORF1
 [Lactococcus lactis] 62 31 171 494 2 1134 1313 gi.vertline.166835 ribulose biphosphate
 carboxylase/oxygenase activase [Arabidopsis 62 37 180 haliana] 518 1 193 882 gi.vertline.153491
 O-methyltransferase [Streptomyces glaucescens] 62 39 690 534 2 369 2522 gi.vertline.1480429 putative
 transcriptional regulator [Bacillus stearothermophilus] 62 35 2154 551 6 4371 4820 gi.vertline.511113 ferric
 uptake regulation protein [Campylobacter jejuni] 62 37 450 574 1 1 570 gi.vertline.153000 enterotoxin B
 [Staphylococcus aureus] 62 43 570 590 2 344 1171 gi.vertline.40367 ORFC [Clostridium acetobutylicum] 62
 37 828 655 1 396 830 gi.vertline.147195 phnB protein [Escherichia coli] 62 44 435 656 1 2 478
 gi.vertline.1205451 cell division inhibitor [Haemophilus influenzae] 62 36 477 676 1 348 4 gi.vertline.1511613
 methyl coenzyme M reductase system, component A2 62 36 345 [Methanococcus jannaschii] 687 1 248 3
 gi.vertline.49272 Asparaginase [Bacillus licheniformis] 62 48 246 700 2 267 944 gi.vertline.1205822
 hypothetical protein (GB:X75627_4) [Haemophilus influenzae] 62 40 678 840 2 1041 367 gi.vertline.1045865
 M. genitalium predicted coding region MG181 [Mycoplasma 62 36 675 genitalium] 864 4 898 1491
 gi.vertline.1144332 deoxyuridine nucleotidohydrolase [Homo sapiens] 62 38 594 916 1 35 400

gi.vertline.413931 ipa-7d gene product [Bacillus subtilis] 62 45 366 1071 1 1 771 gi.vertline.1510649 aspartokinase I [Methanococcus jannaschii] 62 40 771 1084 1 19 609 gi.vertline.688011 AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa] 62 39 591 1103 1 3 203 gi.vertline.581261 ORF homologous to E. coli metB [Herpetosiphon aurantiacus] 62 51 201 pir.vertline.S14030.vertline.S14030 Hypothetical protein - Herpetosiphon aurantiacus (fragment) 1217 1 233 3 gi.vertline.460025 ORF2, putative [Streptococcus pneumoniae] 62 41 231 1533 1 414 184 gi.vertline.413968 ipa-44d gene product [Bacillus subtilis] 62 48 231 1537 1 3 257 gi.vertline.1510641 alanyl-tRNA synthetase [Methanococcus jannaschii] 62 29 255 2287 1 3 161 gi.vertline.485956 mrpC gene product [Proteus mirabilis] 62 45 159 2386 1 3 245 gi.vertline.285708 nontoxic component [Clostridium botulinum] 62 31 243 2484 1 167 3 gi.vertline.142092 DNA-repair protein (recA) [Anabaena variabilis] 62 35 165 2490 1 400 2 gi.vertline.581648 epiB gene product [Staphylococcus epidermidis] 62 42 399 3016 1 300 4 gi.vertline.710022 uroporphyrinogen III [Bacillus subtilis] 62 51 297 3116 1 1 213 gi.vertline.466883 nifS; B1496_C2_193 [Mycobacterium leprae] 62 44 213 3297 1 413 3 gi.vertline.475715 acetyl coenzyme A acetyltransferase (thiolase) [Clostridium 62 42 411 cetobutylicum] 3609 1 31 276 gi.vertline.1408501 homologous to N-acyl-L-amino acid amidohydrolase of Bacillus 62 48 246 stearothermophilus [Bacillus subtilis] 3665 2 402 220 gi.vertline.151259 HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] 62 40 183 pir.vertline.A44756.vertline.A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp. 3733 1 3 374 gi.vertline.1353197 thioredoxin reductase [Eubacterium acidaminophilum] 62 42 372 3898 1 1 237 gi.vertline.153675 tagatose 6-P kinase [Streptococcus mutans] 62 45 237 4027 1 143 3 gi.vertline.330705 homologue to gene 30 (aa 1-59); putative [Bovine herpesvirus 4] 62 43 141 4109 1 365 3 gi.vertline.41748 hsdM protein (AA 1-520) [Escherichia coli] 62 45 363 4303 1 1 303 gi.vertline.1303813 YqeW [Bacillus subtilis] 62 43 303

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc
Image												

☐ 2. Document ID: US 6528289 B1

L5: Entry 2 of 4

File: USPT

Mar 4, 2003

DOCUMENT-IDENTIFIER: US 6528289 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

Detailed Description Paragraph Table (2):

86.7 95.1 285 HI1442 1525823 1526707 famesyldiphosphate synthase (ispA) {Escherichia coli} 53.6 71.2 297 HI0195 206694 208049 o-succinylbenzoate-CoA synthase (menE) {Escherichia coli} 46.0 66.8 426 Heme, porphyrin HI1163 1229908 1228940 ferrochelatase (visA) {Escherichia coli} 51.6 69.4 315 HI0113 119848 122079 heme utilization protein (hxC) {Haemophilus influenzae} 26.4 46.1 695 HI0265 293930 295624 heme-hemopexin utilization (hxB) {Haemophilus influenzae} 98.1 98.9 565 HI0604 631034 629751 hemY protein (hemY) {Escherichia coli} 38.9 64.4 355 HI0465 484621 485769 oxygen-independent coproporphyrinogen III oxidase (hemN) {Salmonella 31.5 52.3 241 typhimurium} HI1204 1267418 1266477 protoporphyrinogen oxidase (hemG) {Escherichia coli} 36.1 56.8 153 HI1565 1629849 1628974 protoporphyrinogen oxidase (hemG) {Escherichia coli} 59.1 72.6 203 HI0605 631035 632562 uroporphyrinogen III methylase (hemX) {Escherichia coli} 39.9 60.3 358 Cell envelope Membranes,

lipoproteins, porins HI1585 1647711 1647247 15 kd peptidoglycan-associated lipoprotein (lpp) {Haemophilus influenzae} 94.8 95.5 154 HI0622 653682 652864 28 kDa membrane protein (hipA) {Haemophilus influenzae} 99.6 100.0 273 HI0304 335684 337249 apolipoprotein N-acyltransferase (cute) {Escherichia coli} 45.2 64.1 497 HI0362 384880 384035 hydrophobic membrane protein {Streptococcus gordonii} 37.2 66.5 268 HI0409 428260 427478 hydrophobic membrane protein {Streptococcus gordonii} 34.4 61.3 254 HI1573 1634553 1636106 iron-regulated outer membrane protein A (iroA) {Neisseria meningitidis} 28.9 50.9 398 HI0695 736825 737646 lipoprotein (hel) {Haemophilus influenzae} 99.6 99.6 274 HI0707 749215 750429 lipoprotein (nlpD) {Escherichia coli} 48.6 64.8 364 HI0705 748419 748994 lipoprotein B (lppB) {Haemophilus somnus} 72.3 89.5 191 HI0895 946675 947916 membrane fusion protein (mtrC) {Neisseria gonorrhoeae} 30.9 53.6 337 HI0403 421547 422923 outer membrane protein P1 (ompP1) {Haemophilus influenzae} 93.0 97.2 459 HI0140 153446 154522 outer membrane protein P2 (ompP2) {Haemophilus influenzae} 96.7 97.5 361 HI1167 1234699 1235757 outer membrane protein P5 (ompA) {Haemophilus influenzae} 94.1 95.8 353 HI0906 958098 958901 prolipoprotein diacylglycerol transferase (lgt) {Escherichia coli} 62.8 80.1 285 HI0030 31698 30838 rare lipoprotein A (rlpA) {Escherichia coli} 34.5 57.8 288 HI0924 979182 979727 rare lipoprotein B (rlpB) {Escherichia coli} 33.5 62.1 163 Surface polysaccharides, lipopolysaccharides & antigens HI1563 1628153 1627302 2-dehydro-3-deoxyphosphooctonate aldolase (kdsA) {Escherichia coli} 81.3 91.5 283 HI0654 696743 695463 3-deoxy-d-manno-octulosonic-acid transferase (kdtA) {Escherichia coli} 50.7 69.9 420 HI1108 1169176 1168139 ADP-heptose-lps heptosyltransferase II (rfaF) {Escherichia coli} 63.6 78.9 345 HI1117 1181141 1180218 ADP-L-glycero-D-mannoheptose-6-epimerase (rfaD) {Escherichia coli} 78.2 87.7 308 HI0058 59659 58898 CTP:CMP-3-deoxy-D-manno-octulosonate-cytidylyl-transferase (kdsB) 65.0 81.7 245 {Escherichia coli} HI0917 970233 969211 firA protein (firA) {Pasteurella multocida} 84.9 91.1 338 HI0870 919974 920723 glycosyl transferase (lgtD) {Neisseria gonorrhoeae} 30.3 55.3 200 HI1584 1646090 1647058 glycosyl transferase (lgtD) {Neisseria gonorrhoeae} 47.3 64.0 328 HI0653 695463 694996 KDTB protein (kdtB) {Escherichia coli} 52.3 75.8 153 HI1684 1746281 1747291 kpsF protein (kpsF) {Escherichia coli} 49.3 70.6 294 HI1543 1607986 1808967 lic-1 operon protein (licA) {Haemophilus influenzae} 99.1 100.0 321 HI1544 1608970 1609885 lic-1 operon protein (licB) {Haemophilus influenzae} 99.0 99.3 303 HI1545 1609845 1610543 lic-1 operon protein (licC) {Haemophilus influenzae} 96.5 99.5 198 HI1546 1610546 1611340 lic-1 operon protein (licD) {Haemophilus influenzae} 88.7 94.0 268 HI1062 1125450 1124254 lipid A disaccharide synthetase (lpxB) {Escherichia coli} 63.2 77.3 382 HI0552 571001 570096 lipooligosaccharide biosynthesis protein {Haemophilus influenzae} 98.3 99.0 298 HI0767 827911 628756 lipooligosaccharide biosynthesis protein {Haemophilus influenzae} 36.4 59.5 267 HI0869 918779 919990 lsg focus hypothetical protein (GB:M94855_1) {Haemophilus influenzae} 60.5 82.5 400 HI1706 1770127 1768916 lsg focus hypothetical protein (GB:M94855_1) {Haemophilus influenzae} 99.3 100.0 401 HI1705 1768916 1768005 lsg focus hypothetical protein (GB:M94855_2) {Haemophilus influenzae} 98.4 98.7 304 HI1704 1768000 1767322 lsg focus hypothetical protein (GB:M94855_3) {Haemophilus influenzae} 96.0 97.4 226 HI1703 1766957 1766157 lsg focus hypothetical protein (GB:M94855_4) {Haemophilus influenzae} 96.1 98.4 257 HI1702 1766142 1765261 lsg focus hypothetical protein (GB:M94855_5) {Haemophilus influenzae} 96.9 98.3 294 HI1701 1765256 1764456 lsg focus hypothetical protein (GB:M94855_6) {Haemophilus influenzae} 98.9 99.3 267 HI1700 1763577 1764341 lsg focus hypothetical protein (GB:M94855_7) {Haemophilus influenzae} 98.4 98.4 255 HI1699 1763439 1762678 lsg focus hypothetical protein (GB:M94855_8) {Haemophilus influenzae} 98.6 99.0 209 HI0263 290317 291357 opsX focus protein (opsX) {Xanthomonas campestris} 35.2 56.7 261 HI1722 1788547 1787483 rfe (CGSC No 294) protein {Escherichia coli} 59.0 77.2 344 HI1147 1212723 1213637 UDP-3-o-acyl N-acetylglucosamine deacetylase (envA) {Escherichia coli} 77.3 88.2 304 HI1063 1126278 1125493 UDP-N-acetylglucosamine acetyltransferase (lpxA) {Escherichia coli} 66.0 79.4 262 HI0875 925083 926096 UDP-N-acetylglucosamine epimerase (rfpE) {Escherichia coli} 65.5 79.5 336 HI0874 923609 925021 undecaprenyl-phosphate galactosephosphotransferase (rfbP) {Salmonella 57.9 75.1 465 typhimurium} Surface structures HI1738 1808251 1804281 adhesin (aidA-I) {Escherichia coli} 29.3 45.8 1196 HI0119 133314 134324 adhesin B precursor (fimA) {Streptococcus parasanguis} 24.5 48.3 309 HI0364 386685 385807 adhesin B precursor (fimA) {Streptococcus parasanguis} 34.6 61.6 302 HI0332 356770 358062 cell envelope protein (oapA) {Haemophilus influenzae} 99.8 100.0 431 HI0713 757120 757425 flagellar switch protein (fliM)

{*Salmonella typhimurium*} 34.1 61.0 41 HI1464 1542848 1542296 invasin precursor (outer membrane adhesin) (yopA) {*Yersinia enterocolitica*} 38.5 62.1 291 HI0333 358125 358526 opacity associated protein (oapB) {*Haemophilus influenzae*} 99.2 99.2 132 HI0416 436627 436836 opacity protein (opa66) {*Neisseria gonorrhoeae*} 74.5 90.9 55 HI1177 1243585 1243947 opacity protein (opa66) {*Neisseria gonorrhoeae*} 37.7 59.0 181 HI1461 1540805 1540272 opacity protein (opaD) {*Neisseria meningitidis*} 34.5 55.8 230 HI0300 333052 331661 pilin biogenesis protein (pilB) {*Pseudomonas aeruginosa*} 44.1 64.8 485 HI0919 973373 970950 protective surface antigen D15 {*Haemophilus influenzae*} 98.6 99.5 797 Murein sacculus, peptidoglycan HI1674 1737564 1735481 carboxy-terminal protease, penicillin-binding protein 3 (prc) {*Escherichia coli*} 52.3 69.5 660 coli} HI1143 1208355 1209272 D-alanine-D-alanine ligase (ddlB) {*Escherichia coli*} 59.9 75.8 303 HI1333 1408286 1406850 D-alanyl-D-alanine carboxypeptidase (dacB) {*Escherichia coli*} 43.9 68.2 454 HI0066 68323 69618 N-acetylmuramoyl-L-alanine amidase (amiB) {*Escherichia coli*} 59.5 77.0 221 HI0383 401990 401532 PC protein (15 kd peptidoglycan-associated outer membrane lipoprotein) 100.0 100.0 153 (pal) {*Haemophilus influenzae*} HI1731 1795566 1797908 penicillin-binding protein 1B (ponB) {*Escherichia coli*} 47.0 67.5 767 HI0032 34810 32858 penicillin-binding protein 2 (pbp2) {*Escherichia coli*} 58.8 73.8 609 HI0029 30819 29641 penicillin-binding protein 5 (dacA) {*Escherichia coli*} 54.8 68.4 362 HI0198 212582 213439 penicillin-insensitive murein endopeptidase (mepA) {*Escherichia coli*} 49.3 66.7 269 HI1138 1201927 1203006 phospho-N-acetylmuramoyl-pentapeptide-transferase E (mraY) {*Escherichia coli*} 76.7 88.9 360 coli} HI0038 40689 41741 rod shape-determining protein (mreC) {*Escherichia coli*} 50.3 74.5 293 HI0031 32865 31753 rod shape-determining protein (mreB) {*Escherichia coli*} 63.1 80.7 358 HI0037 39473 40606 rod shape-determining protein (mreB) {*Escherichia coli*} 79.6 89.9 347 HI0039 41744 42229 rod shape-determining protein (mreD) {*Escherichia coli*} 40.6 71.6 154 HI0831 878792 880570 soluble lytic murein transglycosylase (slt) {*Escherichia coli*} 40.4 59.3 378 HI1141 1205663 1206715 transferase, peptidoglycan synthesis (murG) {*Escherichia coli*} 61.7 76.0 350 HI1137 1200560 1201930 UDP-murNac-pentapeptide synthetase (murF) {*Escherichia coli*} 51.4 68.2 452 HI1136 1199080 1200543 UDP-MurNac-tripeptide synthetase (murE) {*Escherichia coli*} 55.7 72.6 463 HI0270 301245 302267 UDP-N-acetylenolpyruvoylglucosamine reductase (murB) {*Escherichia coli*} 57.6 75.6 340 HI1083 1148434 1147163 UDP-N-acetylglucosamine enolpyruvyl transferase (murZ) {*Escherichia coli*} 72.4 84.5 419 HI1142 1206856 1208280 UDP-N-acetylmuramate-alanine ligase (murC) {*Escherichia coli*} 68.2 81.8 470 HI1139 1203132 1204442 UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD) {*Escherichia coli*} 61.0 73.7 437 HI1499 1569479 1569826 N-acetylmuramoyl-L-alanine amidase {*Bacteriophage T3*} 42.9 62.2 97 Central intermediary metabolism Phosphorus compounds HI0697 739608 738640 exopolyphosphatase (ppx) {*Escherichia coli*} 55.2 76.7 318 HI0124 139861 139334 inorganic pyrophosphatase (ppa) {*Escherichia coli*} 36.3 50.3 157 HI0647 689574 688637 lysophospholipase L2 (pldB) {*Escherichia coli*} 31.2 53.1 317 Sulfur metabolism HI1374 1462019 1461693 desulfovibrio gamma subunit (dsvC) {*Desulfovibrio vulgaris*} 36.0 58.0 99 HI0807 854438 853741 putative arylsulfatase regulatory protein (aslB) {*Escherichia coli*} 47.4 67.0 381 HI0561 578539 577856 sulfite synthesis pathway protein (cysQ) {*Escherichia coli*} 35.9 56.0 205 Polyamine biosynthesis HI0099 106307 107374 nucleotide binding protein (potG) {*Escherichia coli*} 42.6 66.9 340 HI0593 614187 612028 ornithine decarboxylase (speF) {*Escherichia coli*} 66.4 80.2 717 Polysaccharides-(cytoplasmic) HI1360 1436170 1438359 1,4-alpha-glucan branching enzyme (glgB) {*Escherichia coli*} 64.5 80.1 723 HI1362 1440427 1441758 ADP-glucose synthetase (glgC) {*Escherichia coli*} 55.0 74.3 407 HI1364 1443545 1446007 alpha-glucan phosphorylase (glgP) {*Escherichia coli*} 61.1 79.1 609 HI1361 1436456 1440434 glycogen operon protein (glgX) {*Escherichia coli*} 54.3 67.8 501 HI1363 1441869 1443296 glycogen synthase (glgA) {*Escherichia coli*} 56.2 71.2 475 Degradation of polysaccharides HI1359 1434061 1436157 amyloamylase (malQ) {*Escherichia coli*} 40.9 62.0 615 HI1420 1507662 1507063 endochitinase {*Oryza sativa*} 38.9 50.9 106 Amino sugars HI0431 452989 451160 glutamine amidotransferase (glmS) {*Escherichia coli*} 72.1 84.3 609 HI0141 155859 154717 N-acetylglucosamine-6-phosphate deacetylase (nagA) {*Escherichia coli*} 54.5 72.1 376 HI0142 156944 156135 nagB protein (nagB) {*Escherichia coli*} 74.2 88.1 260 Other HI0048 49257 48403 7-alpha-hydroxysteroid dehydrogenase (hdhA) {*Escherichia coli*} 32.4 55.1 244 HI1207 1271536 1270334 acetate kinase (ackA) {*Escherichia coli*} 69.1 83.9 396 HI0951 1009728 1006367 GABA transaminase (gabT) {*Escherichia coli*} 34.4 55.8 420

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Image											

□ 3. Document ID: US 6506581 B1

L5: Entry 3 of 4

File: USPT

Jan 14, 2003

DOCUMENT-IDENTIFIER: US 6506581 B1

TITLE: Nucleotide sequence of the *Haemophilus influenzae* Rd genome, fragments thereof, and uses thereof

Detailed Description Paragraph Table (2):

51.6 69.4 315 HI0113 119848 122079 heme utilization protein (hxC) {*Haemophilus influenzae*} 26.4 46.1 695
 HI0265 293930 295624 heme-hemopexin utilization (hxB) {*Haemophilus influenzae*} 98.1 98.9 565 HI0604
 631034 629751 hemY protein (hemY) {*Escherichia coli*} 38.9 64.4 355 HI0465 484621 485769
 oxygen-independent coproporphyrinogen III oxidase (hemN) {*Salmonella typhimurium*} 31.5 52.3 241 HI1204
 1267418 1266477 protoporphyrinogen oxidase (hemG) {*Escherichia coli*} 36.1 56.8 153 HI1565 1629849
 1628974 protoporphyrinogen oxidase (hemG) {*Escherichia coli*} 59.1 72.6 203 HI0605 631035 632562
 uroporphyrinogen III methylase (hemX) {*Escherichia coli*} 39.9 60.3 358 Cell envelope Membranes,
 lipoproteins, porins HI1585 1647711 1647247 15 kd peptidoglycan-associated lipoprotein (lpp) {*Haemophilus*
influenzae} 94.8 95.5 154 HI0622 653682 652864 28 kDa membrane protein (hlpA) {*Haemophilus influenzae*}
 99.6 100.0 273 HI0304 335684 337249 apolipoprotein N-acyltransferase (cute) {*Escherichia coli*} 45.2 64.1
 497 HI0362 384880 384035 hydrophobic membrane protein {*Streptococcus gordonii*} 37.2 66.5 268 HI0409
 428260 427478 hydrophobic membrane protein {*Streptococcus gordonii*} 34.4 61.3 254 HI1573 1634553
 1636106 iron-regulated outer membrane protein A (iroA) {*Neisseria meningitidis*} 28.9 50.9 398 HI0695
 736825 737646 lipoprotein (hel) {*Haemophilus influenzae*} 99.6 99.6 274 HI0707 749215 750429 lipoprotein
 (nlpD) {*Escherichia coli*} 48.6 64.8 364 HI0705 748419 748994 lipoprotein B (lppB) {*Haemophilus somnus*}
 72.3 89.5 191 HI0896 946675 947916 membrane fusion protein (mtrC) {*Neisseria gonorrhoeae*} 30.9 53.6
 337 HI0403 421547 422923 outer membrane protein P1 (ompP1) {*Haemophilus influenzae*} 93.0 97.2 459
 HI0140 153446 154522 outer membrane protein P2 (ompP2) {*Haemophilus influenzae*} 96.7 97.5 361 HI1167
 1234699 1235757 outer membrane protein P5 (ompA) {*Haemophilus influenzae*} 94.1 95.8 353 HI0906 958098
 958901 prolipoprotein diacylglycerol transferase (lgt) {*Escherichia coli*} 62.8 80.1 285 HI0030 31698 30838
 rare lipoprotein A (rlpA) {*Escherichia coli*} 34.5 57.8 288 HI0924 979182 979727 rare lipoprotein B (rlpB)
 {*Escherichia coli*} 33.5 62.1 163 Surface polysaccharides, lipopolysaccharides & antigens HI1563 1628153
 1627302 2-dehydro-3-deoxyphosphooctonate aldolase (kdsA) {*Escherichia coli*} 81.3 91.5 283 HI0654 696743
 695463 3-deoxy-d-manno-octulosonic-acid transferase (kdtA) {*Escherichia coli*} 50.7 69.9 420 HI1108
 1169176 1168139 ADP-heptose-lps heptosyltransferase II (rfaF) {*Escherichia coli*} 63.6 78.9 345 HI1117
 1181141 1180218 ADP-L-glycero-D-mannoheptose-6-epimerase (rfaD) {*Escherichia coli*} 78.2 87.7 308 HI0058
 59659 58898 CTP: CMP-3-deoxy-D-manno-octulosonate-cytidylyl-transferase (kdsB) {*Escherichia coli*} 65.0
 81.7 245 HI0917 970233 969211 firA protein (firA) {*Pasteurella multocida*} 84.9 91.1 338 HI0870 919974
 920723 glycosyl transferase (lgtD) {*Neisseria gonorrhoeae*} 30.3 55.3 200 HI1584 1646090 1647058 glycosyl
 transferase (lgtD) {*Neisseria gonorrhoeae*} 47.3 64.0 328 HI0653 695463 694996 KDTB protein (kdtB)
 {*Escherichia coli*} 52.3 75.8 153 HI1684 1746281 1747291 kpsF protein (kpsF) {*Escherichia coli*} 49.3 70.6 294

HI1543 1607986 1608967 lic-1 operon protein (licA) {Haemophilus influenzae} 99.1 100.0 321 HI1544
 1608970 1609885 lic-1 operon protein (licB) {Haemophilus influenzae} 99.0 99.3 303 HI1545 1609845
 1610543 lic-1 operon protein (licC) {Haemophilus influenzae} 96.5 99.5 198 HI1546 1610546 1611340 lic-1
 operon protein (licD) {Haemophilus influenzae} 88.7 94.0 268 HI1062 1125450 1124254 lipid A disaccharide
 synthetase (lpxB) {Escherichia coli} 63.2 77.3 382 HI0552 571001 570096 lipooligosaccharide biosynthesis
 protein {Haemophilus influenzae} 98.3 99.0 298 HI0767 827911 828756 lipooligosaccharide biosynthesis
 protein {Haemophilus influenzae} 36.4 59.5 267 HI0869 918779 919990 lsg locus hypothetical protein
 (GB:M94855_1) {Haemophilus influenzae} 60.5 82.5 400 HI1706 1770127 1768916 lsg locus hypothetical
 protein (GB:M94855_1) {Haemophilus influenzae} 99.3 100.0 401 HI1705 1768916 1768005 lsg locus
 hypothetical protein (GB:M94855_2) {Haemophilus influenzae} 98.4 98.7 304 HI1704 1768000 1767322 lsg
 locus hypothetical protein (GB:M94855_3) {Haemophilus influenzae} 96.0 97.4 226 HI1703 1766957 1766157
 lsg locus hypothetical protein (GB:M94855_4) {Haemophilus influenzae} 96.1 98.4 257 HI1702 1766142
 1765261 lsg locus hypothetical protein (GB:M94855_5) {Haemophilus influenzae} 96.9 98.3 294 HI1701
 1765256 1764456 lsg locus hypothetical protein (GB:M94855_6) {Haemophilus influenzae} 98.9 99.3 267
 HI1700 1763577 176341 lsg locus hypothetical protein (GB:M94855_7) {Haemophilus influenzae} 98.4 98.4
 255 HI1699 1763439 1762678 lsg locus hypothetical protein (GB:M94855_8) {Haemophilus influenzae} 98.6
 99.0 209 HI0263 290317 291357 opsX locus protein (opsX) {Xanthomonas campestris} 35.2 56.7 261 HI1722
 1788547 1787483 rfe (CGSC No 294) protein {Escherichia coli} 59.0 77.2 344 HI1147 1212723 1213637
 UDP-3-o-acyl N-acetylglucosamine deacetylase (envA) {Escherichia coli} 77.3 88.2 304 HI1063 1126278
 1125493 UDP-N-acetylglucosamine acetyltransferase (lpxA) {Escherichia coli} 66.0 79.4 262 HI0875 925083
 926096 UDP-N-acetylglucosamine epimerase (rfeE) {Escherichia coli} 65.6 79.5 336 HI0874 923609 925021
 undecaprenyl-phosphate galactosephosphotransferase (rfbP) 57.9 75.1 465 {Salmonella typhimurium} Surface
 structures HI1738 1808251 1804281 adhesin (aidA-I) {Escherichia coli} 29.3 45.8 1196 HI0119 133314 134324
 adhesin B precursor (fimA) {Streptococcus parasanguis} 24.5 48.3 309 HI0364 386685 385807 adhesin B
 precursor (fimA) {Streptococcus parasanguis} 34.6 61.6 302 HI0332 356770 358062 cell envelope protein
 (oapA) {Haemophilus influenzae} 99.8 100.0 431 HI0713 757120 757425 flagellar switch protein (fliM)
 {Salmonella typhimurium} 34.1 61.0 41 HI1464 1542848 1542296 invasin precursor (outer membrane adhesin)
 (yopA) {Yersinia enterocolitica} 38.5 62.1 291 HI0333 358125 358526 opacity associated protein (oapB)
 {Haemophilus influenzae} 99.2 99.2 132 HI0416 436627 436836 opacity protein (opa66) {Neisseria
 gonorrhoeae} 74.5 90.9 55 HI1177 1243585 1243947 opacity protein (opa66) {Neisseria gonorrhoeae} 37.7
 59.0 181 HI1461 1540805 1540272 opacity protein (opaD) {Neisseria meningitidis} 34.5 55.8 230 HI0300
 333052 331661 pilin biogenesis protein (pilB) {Pseudomonas aeruginosa} 44.1 64.8 485 HI0919 973373
 970950 protective surface antigen D15 {Haemophilus influenzae} 98.6 99.5 797 Murein sacculus, peptidoglycan
 HI1674 1737564 1735481 carboxy-terminal protease, penicillin-binding protein 3 (prc) {Escherichia coli} 52.3
 69.5 660 HI1143 1208355 1209272 D-alanine-D-alanine ligase (ddlB) {Escherichia coli} 59.9 75.8 303 HI1333
 1408286 1406850 D-alanyl-D-alanine carboxypeptidase (dacB) {Escherichia coli} 43.9 68.2 454 HI0066 68323
 69618 N-acetylmuramoyl-L-alanine amidase (amiB) {Escherichia coli} 59.5 77.0 221 HI0383 401990 401532 PC
 protein (15kd peptidoglycan-associated outer membrane lipoprotein) (pal) 100.0 100.0 153 {Haemophilus
 influenzae} HI1731 1795566 1797908 penicillin-binding protein 1B (ponB) {Escherichia coli} 47.0 67.5 767
 HI0032 34810 32858 penicillin-binding protein 2 (pbp2) {Escherichia coli} 58.8 73.8 609 HI0029 30819
 29641 penicillin-binding protein 5 (dacA) {Escherichia coli} 54.8 68.4 362 HI0198 212582 213439
 penicillin-insensitive murein endopeptidase (mepA) {Escherichia coli} 49.3 66.7 269 HI1138 1201927 1203006
 phospho-N-acetylmuramoyl-pentapeptide-transferase E (mraY) {Escherichia coli} 76.7 88.9 360 HI0038 40689
 41741 rod shape-determining protein (mreC) {Escherichia coli} 50.3 74.5 293 HI0031 32865 31753 rod
 shape-determining protein (mreB) {Escherichia coli} 63.1 80.7 358 HI0037 39473 40606 rod
 shape-determining protein (mreB) {Escherichia coli} 79.6 89.9 347 HI0039 41744 42229 rod
 shape-determining protein (mreD) {Escherichia coli} 40.6 71.6 154 HI0831 878792 880570 soluble lytic
 murein transglycosylase (slt) {Escherichia coli} 40.4 59.3 378 HI1141 1205663 1206715 transferase,
 peptidoglycan synthesis (murG) {Escherichia coli} 61.7 76.0 350 HI1137 1200560 1201930
 UDP-murac-pentapeptide synthetase (mrF) {Escherichia coli} 51.4 68.2 452 HI1136 1199080 1200543

UDP-MurNac-tripeptide synthetase (murE) {Escherichia coli} 55.7 72.6 463 HI0270 301245 302267
 UDP-N-acetylenolpyruvylglucosamine reductase (murB) {Escherichia coli} 57.6 75.6 340 HI1083 1148434
 1147163 UDP-N-acetylglucosamine enolpyruvyl transferase (murZ) {Escherichia coli} 72.4 84.5 419 HI1142
 1206856 1208280 UDP-N-acetylmuramate-alanine ligase (murC) {Escherichia coli} 68.2 81.8 470 HI1139
 1203132 1204442 UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD) {Escherichia coli} 61.0 73.7 437
 HI1499 156479 1569826 N-acetylmuramoyl-L-alanine amidase {Bacteriophage T3} 42.9 62.2 97 Central
 intermediary metabolism Phosphorus compounds HI0697 739608 738640 exopolyphosphatase (ppx)
 {Escherichia coli} 55.2 76.7 318 HI0124 139861 139334 inorganic pyrophosphatase (ppa) {Escherichia coli}
 36.3 50.3 157 HI0647 689574 688637 lysophospholipase L2 (pldB) {Escherichia coli} 31.2 53.1 317 Sulfur
 metabolism HI1374 1462019 1461693 desulfoviridin gamma subunit (dsvC) {Desulfovibrio vulgaris} 36.0 58.0
 99 HI0807 854438 853741 putative arylsulfatase regulatory protein (aslB) {Escherichia coli} 47.4 67.0 381
 HI0561 578539 577856 sulfite synthesis pathway protein (cysQ) {Escherichia coli} 35.9 56.0 205 Polyamine
 biosynthesis HI0099 106307 107374 nucleotide binding protein (potG) {Escherichia coli} 42.6 66.9 340
 HI0593 614187 612028 ornithine decarboxylase (speF) {Escherichia coli} 66.4 80.2 717 Polysaccharides -
 (cytoplasmic) HI1360 1436170 1438359 1,4-alpha-glucan branching enzyme (glgB) {Escherichia coli} 64.5 80.1
 723 HI1362 1440427 1441758 ADP-glucose synthetase (glgC) {Escherichia coli} 55.0 74.3 407 HI1364
 1443545 1446007 alpha-glucan phosphorylase (glgP) {Escherichia coli} 61.1 79.1 809 HI1361 1438458 1440434
 glycogen operon protein (glgX) {Escherichia coli} 54.3 67.8 501 HI1363 1441869 1443296 glycogen synthase
 (glgA) {Escherichia coli} 56.2 71.2 475 Degradation of polysaccharides HI1359 1434061 1436157 amylomaltase
 (malQ) {Escherichia coli} 40.9 62.0 615 HI1420 1507662 1507063 endochitinase {Oryza sativa} 38.9 50.9 106
 Amino sugars HI0431 452989 451160 glutamine amidotransferase (glmS) {Escherichia coli} 72.1 84.3 609
 HI0141 155859 154717 N-acetylglucosamine-6-phosphate deacetylase (nagA) {Escherichia coli} 54.5 72.1 376
 HI0142 156944 156135 nagB protein (nagB) {Escherichia coli} 74.2 88.1 260 Other HI0048 49257 48403
 7-alpha-hydroxysteroid dehydrogenase (hdhA) {Escherichia coli} 32.4 55.1 244 HI1207 1271536 1270334
 acetate kinase (ackA) {Escherichia coli} 69.1 83.9 396 HI0951 1009728 1008367 GABA transaminase (gabT)
 {Escherichia coli} 34.4 55.8 420 HI0111 118858 119484 glutathione transferase (bphH) {Pseudomonas sp.} 37.6
 57.4 200 HI0693 734488 735996 glycerol kinase (glpK) {Escherichia coli} 76.9 89.2 502 HI0586 606429
 605161 hippuricase (hipO) {Campylobacter jejuni} 27.8 49.6 376 HI0543 564874 564575 urease (ureA)
 {Helicobacter heilmannii} 62.4 76.2 101 HI0539 561668 561087 urease accessory protein (UreF) {Bacillus sp.}
 31.8 54.9 194 HI0541 564179 562464 urease alpha subunit (urea amidohydrolase)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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☐ 4. Document ID: US 6211161 B1

L5: Entry 4 of 4

File: USPT

Apr 3, 2001

DOCUMENT-IDENTIFIER: US 6211161 B1

TITLE: UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (MURD) of staphylococcus aureus

Brief Summary Text (7):

UDP-N-acetylmuramoylalanine-D-glutamate ligase (D-glutamate adding enzyme) is one of the enzymes involved

in the biosynthesis of peptidoglycan. It catalyses the addition of D-glutamate to UDP-N-acetylmuramoyl-L-alanine. This is coupled to the cleavage of ATP into ADP and inorganic phosphate (El-Sherbeini, M., Geissler, W. M., Pittman, J., Yuan, X., Wong, K. K., and Pompliano, D. L. (1998) Cloning and expression of *Staphylococcus aureus* and *Streptococcus pyogenes* murD genes encoding uridine diphosphate N-acetylmuramoyl-L-alanine:D-glutamate ligases, *Gene* 210:117-125; Mengin-Lecreulx, D. and van Heijenoort, J. (1990) Nucleotide sequence of the murD gene encoding the UDP-MurNAc-L-Ala-D-Glu synthetase of *Escherichia coli*. *Nucleic Acids Research* 18:183). Discovery of a *Staphylococcus aureus* gene encoding a UDP-N-acetylmuramoylalanine-D-glutamate ligase-like protein which is expressed in vivo implies that there is a role for this protein during infection.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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